

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA
<120> Prophylactic or therapeutic agent for blood
coagulation-related diseases
<130> H795-PCT
<160> 104
<210> 1
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer MHC-G1
<400> 1
ggatcccggg ccagtggata gacagatg 28
<210> 2
<211> 27
<212> DNA
<213> Artificial Sequence
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<223> Primer MKC
<400> 2
ggatcccggg tggatggtgg gaagatg 27
<210> 3
<211> 17
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<223> M13 Primer M4
<400> 3
gttttcccag tcacgac 17
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<223> M13 Primer RV

<400> 4

caggaaacag ctatgac

17

<210> 5

<211> 408

<212> DNA

<213> Mouse

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(408)

<223> Nucleotide sequence coding for H chain V region of
anti-TF mouse monoclonal antibody ATR-5

<400> 5

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtc aat tca gag gtt cag ctg cag cag tct ggg act aac ctt gtg agg	96
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Asn Leu Val Arg	
1 5 10	
cca ggg gcc tta gtc aag ttg tcc tgc aaa ggt tct ggc ttc aac att	144
Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Gly Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg	192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu	
30 35 40 45	
gag tgg att gga ggg aat gat cct gcg aat ggt cat agt atg tat gac	240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	
ccg aaa ttc cag ggc aag gcc agt ata aca gca gac aca tcc tcc aac	288
Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn	
65 70 75	

aca gcc tac ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc 336
 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val

80

85

90

tat ttc tgt gct aga gac tcg ggc tat gct atg gac tac tgg ggt caa 384
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln

95

100

105

gga acc tca gtc acc gtc tcc tca 408

Gly Thr Ser Val Thr Val Ser Ser

110

115

<210> 6

<211> 381

<212> DNA

<213> Mouse

<220>

<221> sig-peptide

<222> (1)...(60)

<220>

<221> mat-peptide

<222> (61)...(381)

<223> Nucleotide sequence coding for L chain V region of
 anti-TF mouse monoclonal antibody ATR-5

<400> 6

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro

-20

-15

-10

-5

ggg atc aga tgt gac atc aag atg acc cag tct cca tcc tct atg tat 96

Gly Ile Arg Cys Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr

1

5

10

gca tcg ctg gga gag aga gtc act atc act tgc aag gcg agt cag gac 144

Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp

15

20

25

att aaa agc ttt tta agt tgg tac cag caa aaa cca tgg aaa tct cct 192

Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro

30

35

40

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aag acc ctg atc tat tat gca aca agc ttg gca gat ggg gtc cca tca 240
Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
 45              50              55              60
aga ttc agt ggc agt gga tct ggg caa gat tat tct cta acc atc aac 288
Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn
      65              70              75
aac ctg gag tct gac gat aca gca act tat tat tgt cta cag cat ggt 336
Asn Leu Glu Ser Asp Asp Thr Ala Thr Tyr Tyr Cys Leu Gln His Gly
      80              85              90
gag agc ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 381
Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
      95              100              105

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<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer ch5HS

<400> 7

gtctgtcgac ccaccatgaa atgcagctgg gtcac 35

<210> 8

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer ch5HA

<400> 8

tggttgctagc tgaggagacg gtgactga 28

<210> 9

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer ch5LS

<400> 9

gtctagatct ccaccatgag ggccccctgct cagtt 35

<210> 10
 <211> 28
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer ch5LA
 <400> 10
 tgttctgtacg ttttatttcc agcttggt 28
 <210> 11
 <211> 104
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> CDR grafting primer hr5Hv1S
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 ttctgtcgac ccaccatgaa atgcagctgg gtcattcttct tcctgatggc agtggttaca 60
 ggggttaact cacaggtgca gctgttgagg tctggagctg tgct 104
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 <212> DNA
 <213> Artificial Sequence
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 <223> CDR grafting primer hr5Hv28
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 ctctgcaag gcttcgggat tcaacattaa agactactat atgcattg 108
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 <212> DNA
 <213> Artificial Sequence
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 <223> CDR grafting primer hr5Hv4S
 <400> 13
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 atccgccagt attgcctact tggagttctc ggcctgaca aatgagga 108

<210> 14
 <211> 110
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> CDR grafting primer hr5Hv3A
 <400> 14
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 ggccctctgtt ttacccaatg catatagtag totttaatgt tgaatccgga 110
 <210> 15
 <211> 110
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> CDR grafting primer hr5Hv5A
 <400> 15
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 ccgagtctct tgcacagtaa tagaccgcag aatcctcatt tgtcaggctc 110
 <210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer hr5HvPrS
 <400> 16
 ttctgtcgac ccaccatga 19
 <210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer hr5HvPrA
 <400> 17
 agaagctagc tgaggagac 19
 <210> 18

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(415)

<223> Nucleotide sequence coding for version "a" of
humanized H chain V region

<400> 18

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg	96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg	
1 5 10	
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att	144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta	192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
30 35 40 45	
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac	240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	
ccg aaa ttc cag ggc agg gcc aaa ctg act gca gcc aca tcc gcc agt	288
Pro Lys Phe Gln Gly Arg Ala Lys Leu Thr Ala Ala Thr Ser Ala Ser	
65 70 75	
att gcc tac ttg gag ttc tcg agc ctg aca aat gag gat tct gcg gtc	336
Ile Ala Tyr Leu Glu Phe Ser Ser Leu Thr Asn Glu Asp Ser Ala Val	
80 85 90	
tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa	384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln	
95 100 105	

ggc acc ctg gtc acc gtc tcc tca gct agc

415

Gly Thr Leu Val Thr Val Ser Ser Ala Ser

110

115

<210> 19

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "a" of humanized H chain V region

<400> 19

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr

20

25

30

Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe

50

55

60

Gln Gly Arg Ala Lys Leu Thr Ala Ala Thr Ser Ala Ser Ile Ala Tyr

65

70

75

80

Leu Glu Phe Ser Ser Leu Thr Asn Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser Ala Ser

115

<210> 20

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3RFFS

<400> 20

ttcttggcca tagtatgtat gacccgaaat tccagggccg agtcacaatc actgcagaca 60

catccacgaa cacagcctac atggagctct cgagtctgag

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<210> 21

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3RFBS

<400> 21

ggagctctcg agtctgagat ctgaggacac agccatttat tactgtgcaa gagactcggg 60
ctatgccatg gttct 75

<210> 22

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3RFFA

<400> 22

ctcagactcg agagctccat gtaggctgtg ttctgtgatg tgtctgcagt gattgtgact 60
cggccctgga atttogggtc atacatacta tggccaagaa 100

<210> 23

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3RFBA

<400> 23

agaaccatgg catagcccca gtctcttgca cagtaataaa tggctgtgtc ctcagatctc 60
agactcgaga gctcc 75

<210> 24

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3NMFS

<400> 24

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catccaagaa ccagttctcc ctgaggetct cgagtgtgac 100
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 <211> 75
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3NMBS
 <400> 25
 gaggctctcg agtgtgacag ccgcggacac agccgtatat tactgtgcaa gagactcggg 60
 ctatgccatg gttct 75
 <210> 26
 <211> 100
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3NMFA
 <400> 26
 gtcacactcg agagcctcag ggagaactgg ttcttgatg tgtctaccag cattgtgact 60
 cggccctgga atttcgggtc atacatacta tggccaagaa 100
 <210> 27
 <211> 75
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3NMBA
 <400> 27
 agaaccatgg catagccoga gtctcttgca cagtaatata cggtgtgtgc cgcggctgtc 60
 aactcgaga gcctc 75
 <210> 28
 <211> 414
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> sig-peptide
 <222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "b" of
humanized H chain V region

<400> 28

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

-15

-10

-5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg

1

5

10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile

15

20

25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu

30

35

40

45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp

50

55

60

ccg aaa ttc cag ggc cga gtc aca atc act gca gac aca tcc acg aac 288

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn

65

70

75

aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac aca gcc att 336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile

80

85

90

tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384

Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln

95

100

105

ggc acc ctg gtc acc gtc tcc tca gct agc 414

Gly Thr Leu Val Thr Val Ser Ser Ala Ser

110

115

<210> 29

<211> 119

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Amino acid sequence of version "b" of humanized H chain V region

<400> 29

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser
115

<210> 30

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1) ... (57)

$\langle 220 \rangle$

<221> mat-peptide

 $\langle 222 \rangle \quad (58) \dots (414)$

<223> Nucleotide sequence coding for version "c" of humanized H chain V region

<400> 30

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
-15 -10 -5

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gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg      96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
      1              5              10
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att      144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
      15              20              25
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta      192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
      30              35              40              45
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac      240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
      50              55              60
ccg aaa ttc cag ggc cga gtc aca atg ctg gta gac aca tcc aag aac      288
Pro Lys Phe Gln Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
      65              70              75
cag ttc tcc ctg agg ctc tcg agt gtg aca gcc gcg gac aca gcc gta      336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
      80              85              90
tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa      384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95              100              105
ggc acc ctg gtc acc gtc tcc tca gct agc                                414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110              115

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<210> 31

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "c" of humanized H
chain V region

<400> 31

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Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
      1              5              10              15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
      20              25              30

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Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80
 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser
 115

<210> 32

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3EPS

<400> 32

ttcttgGCCa tagtatgtat gaccogaaat tccagggcag agtcacgatt actgcggacg 60
 aatccacgag cacagcctac atggagctct cgagtctgag 100

<210> 33

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3EPA

<400> 33

agaaccatgg catagcccga gtctctogca cagaaatata cggccgagtc ctcagatctc 60
 agactcgaga gctcc 75

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer F3PrS

<400> 34
 ttcttgcca tagtatgtat 20
 <210> 35
 <211> 18
 <212> DNA
 <213> Artificial Sequence
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 <223> Primer F3PrA
 <400> 35
 agaaccatgg catagccc 18
 <210> 36
 <211> 100
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3VHS
 <400> 36
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 agtcaacgaa gatagcctac atggagctca acagtctgag 100
 <210> 37
 <211> 75
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3VHA
 <400> 37
 agaaccatgg catagccoga gtctctcgca cagaaataaa cggccgtgtc ctcagatctc 60
 agactgttga gctcc 75
 <210> 38
 <211> 414
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> sig-peptide
 <222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "d" of
humanized H chain V region

<400> 38

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Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
      -15              -10              -5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg      96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
      1              5              10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att      144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
      15              20              25

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta      192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
      30              35              40              45

gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac      240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
      50              55              60

cog aaa ttc cag ggc aga gtc acg att act gcg gac gaa tcc acg agc      288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
      65              70              75

aca gcc tac atg gag ctc tog agt ctg aga tct gag gac tcg gcc gta      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
      80              85              90

tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa      384
Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95              100              105

ggc acc ctg gtc acc gtc tcc tca gct agc      414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
      110              115

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<210> 39

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "d" of humanized H chain

<400> 39

Gln	Val	Gln	Leu	Leu	Glu	Ser	Gly	Ala	Val	Leu	Ala	Arg	Pro	Gly	Thr
1				5					10					15	
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Tyr
		20						25					30		
Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Gly	Asn	Asp	Pro	Ala	Asn	Gly	His	Ser	Met	Tyr	Asp	Pro	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
	65				70					75				80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
			85						90				95		
Ala	Arg	Asp	Ser	Gly	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
		100						105					110		
Val	Thr	Val	Ser	Ser	Ala	Ser									
		115													

<210> 40

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "e" of humanized H chain V region

<400> 40

atg	aaa	tgc	agc	tgg	gtc	atc	ttc	ttc	ctg	atg	gca	gtg	gtt	aca	ggg	48
Met	Lys	Cys	Ser	Trp	Val	Ile	Phe	Phe	Leu	Met	Ala	Val	Val	Thr	Gly	
				-15					-10					-5		

```

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg      96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
      1              5              10
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att      144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
      15              20              25
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta      192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
      30              35              40              45
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac      240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
      50              55              60
ccg aaa ttc cag ggc aga gtc tcg att acc gcg gac gag tca acg aag      288
Pro Lys Phe Gln Gly Arg Val Ser Ile Thr Ala Asp Glu Ser Thr Lys
      65              70              75
ata gcc tac atg gag ctc aac agt ctg aga tct gag gac acg gcc gtt      336
Ile Ala Tyr Met Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Val
      80              85              90
tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa      384
Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95              100              105
ggc acc ctg gtc acc gtc tcc tca gct agc                                414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
      110              115

```

<210> 41

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "e" of humanized H
chain V region

<400> 41

```

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
      1              5              10              15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
      20              25              30

```

Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
 50 55 60
 Gln Gly Arg Val Ser Ile Thr Ala Asp Glu Ser Thr Lys Ile Ala Tyr
 65 70 75 80
 Met Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser

115

<210> 42

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3SSS

<400> 42

ttcttgcca tagtatgtat gacccgaaat tccagggcag agtcacgatt accgcggaca 60
 catccacgag cacagcctac atggagctca ggagcctgag 100

<210> 43

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3SSA

<400> 43

agaaccatgg catagccga gtctctcgca cagtaataca cggccgtgtc gtcagatctc 60
 aggctcctga gctcc 75

<210> 44

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3CDS

<400> 44

ttcttgcca tagtatgtat gaccgaaat tccagggcaa agccactctg actgcagacg 60
aatcctccag cacagcctac atgcaactct cgagcctacg 100

<210> 45

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3CDA

<400> 45

agaaccatgg catagcccga gtctcttgca caagaataga ccgcagagtc ctcagatcgt 60
aggctcgaga gttgc 75

<210> 46

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "f" of
humanized H chain V region

<400> 46

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

-15

-10

-5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg

1

5

10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile

15

20

25

```

aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 30          35          40          45
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
          50          55          60
ccg aaa ttc cag ggc aga gtc acg att acc gcg gac aca tcc acg agc 288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
          65          70          75
aca gcc tac atg gag ctc agg agc ctg aga tct gac gac acg gcc gtg 336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
          80          85          90
tat tac tgt gcg aga gac tog ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
          95          100          105
ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110          115

```

<210> 47

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "f" of humanized H
chain V region

<400> 47

```

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
 1          5          10          15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
          20          25          30
Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
          35          40          45
Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
          50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
          65          70          75          80

```

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser
 115

<210> 48

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "g" of
 humanized H chain V region

<400> 48

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg	96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg	
1 5 10	
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att	144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta	192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
30 35 40 45	
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac	240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	

```

ccg aaa ttc cag ggc aaa gcc act ctg act gca gac gaa tcc tcc agc 288
Pro Lys Phe Gln Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser
      65              70              75
aca gcc tac atg caa ctc tcg agc cta cga tct gag gac tct gcg gtc 336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val
      80              85              90
tat tct tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Ser Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95              100             105
ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110              115

```

<210> 49

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "g" of humanized H
chain V region

<400> 49

```

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
  1              5              10              15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
      20              25              30
Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
      35              40              45
Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
      50              55              60
Gln Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
      65              70              75              80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Ser Cys
      85              90              95
Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
      100             105             110
Val Thr Val Ser Ser Ala Ser
      115
<210> 50

```

<211> 100
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3ADS
 <400> 50
 ttcttgcca tagtatgtat gaccogaaat tccagggccg cgtcaccatg tcagccgaca 60
 agtcctccag cgccgcctat ttacagtgga ccagccttaa 100
 <210> 51
 <211> 75
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR Shuffling primer F3ADA
 <400> 51
 agaaccatgg catagcccga gtctctcgcg cagaaatata tggcgggtgc cgaggcctta 60
 aggctgggtcc actgt 75
 <210> 52
 <211> 414
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> sig-peptide
 <222> (1)...(57)
 <220>
 <221> mat-peptide
 <222> (58)...(414)
 <223> Nucleotide sequence coding for version "h" of
 humanized H chain
 <400> 52
 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
 -15 -10 -5
 gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
 Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg
 1 5 10


```

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile
    15                20                25
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta 192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    30                35                40                45
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
                50                55                60
ccg aaa ttc cag ggc cgc gtc acc atg tca gcc gac aag tcc tcc agc 288
Pro Lys Phe Gln Gly Arg Val Thr Met Ser Ala Asp Lys Ser Ser Ser
                65                70                75
gcc gcc tat tta cag tgg acc agc ctt aag gcc tcg gac acc gcc ata 336
Ala Ala Tyr Leu Gln Trp Thr Ser Leu Lys Ala Ser Asp Thr Ala Ile
                80                85                90
tat ttc tgc gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
                95                100                105
ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110                115

```

<210> 53

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "h" of humanized H
chain V region

<400> 53

```

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
    1                5                10                15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
                20                25                30
Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
                35                40                45
Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
                50                55                60

```

Gln Gly Arg Val Thr Met Ser Ala Asp Lys Ser Ser Ser Ala Ala Tyr
 65 70 75 80
 Leu Gln Trp Thr Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr Phe Cys
 85 90 95
 Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser
 115

<210> 54

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3MMS

<400> 54

ttcttgcca tagtatgtat gaccgaaat tccagggcag agtcacgatt accgcggaca 60
 catcgacgag cacagtcttc atggaactga gcagcctgag 100

<210> 55

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3MMA

<400> 55

agaaccatgg catagcccga gtctctcgca cagtaataca cggcogtgtc ttcagatctc 60
 aggtgctca gttcc 75

<210> 56

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3BMS

<400> 56

ttcttgcca tagtatgtat gaccgaaat tccagggcag agtcaccttt accgcggaca 60
 catccgcgaa cacagcctac atggagttga ggagcctcag 100

<210> 57

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> FR Shuffling primer F3BMA

<400> 57

agaaccatgg catagcccga gtctctcgca caataataaa cagccgtgtc tgcagatctg 60
aggctcctca actcc 75

<210> 58

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "i" of
humanized H chain V region

<400> 58

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg	96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg	
1 5 10	
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att	144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta	192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
30 35 40 45	
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac	240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	

```

ccg aaa ttc cag ggc aga gtc acg att acc gcg gac aca tcg acg agc 288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
      65              70              75
aca gtc ttc atg gaa ctg agc agc ctg aga tct gaa gac acg gcc gtg 336
Thr Val Phe Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
      80              85              90
tat tac tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95              100             105
ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110              115

```

<210> 59

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "i" of humanized H
chain V region

<400> 59

```

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
  1              5              10              15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
      20              25              30
Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
      35              40              45
Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
      50              55              60
Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Val Phe
      65              70              75              80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
      85              90              95
Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
      100             105             110
Val Thr Val Ser Ser Ala Ser
      115

```

<210> 60

<211> 414
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> sig-peptide
 <222> (1)...(57)
 <220>
 <221> mat-peptide
 <222> (58)...(414)
 <223> Nucleotide sequence coding for version "j" of
 humanized H chain V region
 <400> 60

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg	48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly	
-15 -10 -5	
gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg	96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg	
1 5 10	
cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att	144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile	
15 20 25	
aaa gac tac tat atg cat tgg gta aaa cag agg cct gga cag ggt cta	192
Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
30 35 40 45	
gaa tgg att ggt ggg aat gat cct gcg aat ggc cat agt atg tat gac	240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp	
50 55 60	
ccg aaa ttc cag ggc aga gtc acc ttt acc gcg gac aca tcc gcg aac	288
Pro Lys Phe Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn	
65 70 75	
aca gcc tac atg gag ttg agg agc ctc aga tct gca gac acg gct gtt	336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Val	
80 85 90	
tat tat tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa	384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln	
95 100 105	

ggc acc ctg gtc acc gtc tcc tca gct agc

414

Gly Thr Leu Val Thr Val Ser Ser Ala Ser

110

115

<210> 61

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "j" of humanized H chain V region

<400> 61

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr

20

25

30

Tyr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe

50

55

60

Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr

65

70

75

80

Met Glu Leu Arg Ser Leu Arg Ser Ala Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser Ala Ser

115

<210> 62

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F2MPS

<400> 62

ttctatgcat tgggtgcgcc aggctccagg acagggcctg gagggaatga 60

tcctgcgaat ggccattct

79

<210> 63

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F2MPA

<400> 63

agaatggcca ttgcaggat cattccctcc catccactcc aggccctgtc ctggagcctg 60

gcgcacccaa tgcataa 79

<210> 64

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "b1" of
humanized H chain V region

<400> 64

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

-15

-10

-5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg

1

5

10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile

15

20

25

aaa gac tac tat atg cat tgg gtg cgc cag gct cca gga cag ggc ctg 192

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

30

35

40

45

```

gag tgg atg gga ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Met Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
      50                      55                      60
ccg aaa ttc cag ggc cga gtc aca atc act gca gac aca tcc acg aac 288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn
      65                      70                      75
aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac aca gcc att 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
      80                      85                      90
tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95                      100                      105
ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110                      115

```

<210> 65

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "b1" of humanized H chain V region

<400> 65

```

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
  1              5              10              15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
      20              25              30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
      35              40              45
Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
      50              55              60
Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
      65              70              75              80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
      85              90              95
Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
      100              105              110

```


Val Thr Val Ser Ser Ala Ser

115

<210> 66

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "d1" of
humanized H chain V region

<400> 66

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

-15

-10

-5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg

1

5

10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile

15

20

25

aaa gac tac tat atg cat tgg gtg cgc cag gct cca gga cag ggc ctg 192

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

30

35

40

45

gag tgg atg gga ggg aat gat cct gcg aat ggc cat agt atg tat gac 240

Glu Trp Met Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp

50

55

60

ccg aaa ttc cag ggc aga gtc acg att act gcg gac gaa tcc acg agc 288

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser

65

70

75

aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac tcg gcc gta 336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val

80

85

90

tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
 95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser
 110 115

<210> 67

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "d1" of humanized H
 chain V region

<400> 67

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser
 115

<210> 68

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F2VHS

<400> 68

ttctatgcat tgggtgacgac aggccctctg acaagggtt gagtggattg gagggaatga 60
tcctgcgaat ggccatctt 79

<210> 69

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F2VHA

<400> 69

aagatggcca ttcgcaggat cattccctcc aatccactca agcccttgct caggggcctg 60
tcgcacccaa tgcataaaa 79

<210> 70

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "b3" of
humanized H chain V region

<400> 70

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

-15

-10

-5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96
Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg

1

5

10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144
Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile

15

20

25

```

aaa gac tac tat atg cat tgg gtg cga cag gcc cct gga caa ggg ctt 192
Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30                35                40                45
gag tgg att gga ggg aat gat cct gcg aat ggc cat agt atg tat gac 240
Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
      50                55                60
ccg aaa ttc cag ggc cga gtc aca atc act gca gac aca tcc acg aac 288
Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn
      65                70                75
aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac aca gcc att 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
      80                85                90
tat tac tgt gca aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
Tyr Tyr Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
      95                100                105
ggc acc ctg gtc acc gtc tcc tca gct agc 414
Gly Thr Leu Val Thr Val Ser Ser Ala Ser
110                115

```

<210> 71

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "b3" of humanized H chain V region

<400> 71

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Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
 1                5                10                15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
      20                25                30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
      35                40                45
Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
      50                55                60
Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
      65                70                75                80

```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys

85

90

95

Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser Ala Ser

115

<210> 72

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(57)

<220>

<221> mat-peptide

<222> (58)...(414)

<223> Nucleotide sequence coding for version "d3" of
humanized H chain V region

<400> 72

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly

-15

-10

-5

gtt aac tca cag gtg cag ctg ttg gag tct gga gct gtg ctg gca agg 96

Val Asn Ser Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg

1

5

10

cct ggg act tcc gtg aag atc tcc tgc aag gct tcc gga ttc aac att 144

Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile

15

20

25

aaa gac tac tat atg cat tgg gtg cga cag gcc cct gga caa ggg ctt 192

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

30

35

40

45

gag tgg att gga ggg aat gat cct gcg aat ggc cat agt atg tat gac 240

Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp

50

55

60

ccg aaa ttc cag ggc aga gtc acg att act gcg gac gaa tcc acg agc 288
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser

65 70 75

aca gcc tac atg gag ctc tcg agt ctg aga tct gag gac tcg gcc gta 336
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val

80 85 90

tat ttc tgt gcg aga gac tcg ggc tat gcc atg gac tac tgg ggc caa 384
 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln

95 100 105

ggc acc ctg gtc acc gtc tcc tca gct agc 414
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser

110 115

<210> 73

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "d3" of humanized H
 chain V region

<400> 73

Gln Val Gln Leu Leu Glu Ser Gly Ala Val Leu Ala Arg Pro Gly Thr
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp Pro Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser

115

<210> 74

<211> 98

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling vector h5Lv1S

<400> 74

gtctagatct ccaccatgag ggccctgct cagttttttg ggatcttggt gctctgggtt 60

ccagggatcc gatgtgacat ccagatgacc cagtctcc 98

<210> 75

<211> 98

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling vector h5Lv4S

<400> 75

ttggcagatg ggggccatc aagggtcagt ggctccggat ctggtaccga tttcaactctc 60

accatctcga gtctgcaacc tgaagatttt gcaactta 98

<210> 76

<211> 98

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling vector h5Lv2A

<400> 76

cttaagaagc ttttaatgtc ctgtgaggcc ttgcacgtga tgggtgactct gtctcctaca 60

gatgcagaca gggaggatgg agactgggtc atctggat 98

<210> 77

<211> 98

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling vector h5Lv3A

<400> 77

gatgggaccc catctgcca actagttgca taatagatca ggagcttagg ggctttccct 60

ggttttctgct gataccaact taagaagctt ttaatgtc 98

<210> 78
 <211> 94
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR shuffling vector h5Lv5A
 <400> 78
 tgttcgtacg tttgatctcc accttggtcc ctccgcgaa cgtgtacggg ctctcaccat 60
 gctgcagaca gtagtaagtt gcaaaatctt cagg 94
 <210> 79
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer h5LvS
 <400> 79
 gtctagatct ccaccatgag 20
 <210> 80
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer h5LvA
 <400> 80
 tgttcgtacg tttgatctc 19
 <210> 81
 <211> 381
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> sig-peptide
 <222> (1)...(60)
 <220>
 <221> mat-peptide
 <222> (61)...(381)

<223> Nucleotide sequence coding for version "a" of
humanized L chain V region

<400> 81

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca	48
Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro	
-20 -15 -10 -5	
ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct	96
Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser	
1 5 10	
gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac	144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp	
15 20 25	
att aaa agc ttc tta agt tgg tat cag cag aaa cca ggg aaa gcc cct	192
Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro	
30 35 40	
aag ctc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca	240
Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser	
45 50 55 60	
agg ttc agt ggc tcc gga tct ggt acc gat ttc act ctc acc atc tcg	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser	
65 70 75	
agt ctg caa cct gaa gat ttt gca act tac tac tgt ctg cag cat ggt	336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly	
80 85 90	
gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa	381
Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys	
95 100 105	

<210> 82

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "a" of humanized L
chain V region

<400> 82

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Phe
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 83

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F3SS

<400> 83

gtctggtacc gattacactc tcaccatctc gagcctccag cctgaagatt ttgcaactta 60
 ctattgtctg cagaaca 77

<210> 84

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F3SA

<400> 84

tggtctgcag acaatagtaa gttgcaaaat cttcaggctg gaggctcgag atggtgagag 60
 tgtaatcggt accagac 77

<210> 85

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F3RS

<400> 85

gtctggtacc gattacactc tcaccatctc gagcctccag cctgaagata ttgcaactta 60

ctattgtctg cagaaca 77

<210> 86

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F3RA

<400> 86

tgttctgcag acaatagtaa gttgcaatat cttcaggctg gaggctcgag atggtgagag 60

tgtaatcggt accagac 77

<210> 87

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(60)

<220>

<221> mat-peptide

<222> (61)...(381)

<223> Nucleotide sequence coding for version "b" of
humanized L chain V region

<400> 87

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48

Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro

-20 -15 -10 -5

ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96

Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser

1 5 10

gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac 144

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp

15

20

25

```

att aaa agc ttc tta agt tgg tat cag cag aaa cca ggg aaa gcc cct 192
Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    30                35                40
aag ctc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca 240
Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
    45                50                55                60
agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                65                70                75
agc ctc cag cct gaa gat ttt gca act tac tat tgt ctg cag cat ggt 336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
                80                85                90
gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
    95                100                105

```

<210> 88

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "b" of humanized L chain V region

<400> 88

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
    1                5                10                15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Phe
                20                25                30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
                35                40                45
Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
                50                55                60
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
                65                70                75                80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Tyr
                85                90                95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                100                105

```

<210> 89

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(60)

<220>

<221> mat-peptide

<222> (61)...(381)

<223> Nucleotide sequence coding for version "c" of
humanized L chain V region

<400> 89

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca	48
Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro	
-20 -15 -10 -5	
ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct	96
Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser	
1 5 10	
gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac	144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp	
15 20 25	
att aaa agc ttc tta agt tgg tat cag cag aaa cca ggg aaa gcc cct	192
Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro	
30 35 40	
aag ctc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca	240
Lys Leu Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser	
45 50 55 60	
agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser	
65 70 75	
agc ctc cag cct gaa gat att gca act tac tat tgt ctg cag cat ggt	336
Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln His Gly	
80 85 90	

gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

95

100

105

<210> 90

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "c" of humanized L
 chain V region

<400> 90

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Phe

20

25

30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Tyr

85

90

95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100

105

<210> 91

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> FR shuffling primer F2SS

<400> 91

gtctcttaag ttggttcag cagaaaccag ggaaatctcc taagaccctg atctactatg 60

caactagtaa ca

72

<210> 92

<211> 72

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR shuffling primer F2SA
 <400> 92
 tggtactagt tgcatagtatg atcaggggtct taggagattt ccctgggttc tgctggaacc 60
 aacttaagag ac 72
 <210> 93
 <211> 72
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR shuffling primer F2XS
 <400> 93
 gtctottaag ttggtatcag cagaaaccag agaaagcccc taagtccttg atctattatg 60
 caactagtaa ca 72
 <210> 94
 <211> 72
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> FR shuffling primer F2XA
 <400> 94
 tggtactagt tgcataatag atcaggggact taggggcttt ctctgggttc tgctgatacc 60
 aacttaagag ac 72
 <210> 95
 <211> 381
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> sig-peptide
 <222> (1)...(60)
 <220>
 <221> mat-peptide
 <222> (61)...(381)

<223> Nucleotide sequence coding for version "b1" of
humanized L chain V region

<400> 95

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca	48
Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro	
-20 -15 -10 -5	
ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct	96
Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser	
1 5 10	
gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac	144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp	
15 20 25	
att aaa agc ttc tta agt tgg ttc cag cag aaa cca ggg aaa tct cct	192
Ile Lys Ser Phe Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro	
30 35 40	
aag acc ctg atc tac tat gca act agt ttg gca gat ggg gtc cca tca	240
Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser	
45 50 55 60	
agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser	
65 70 75	
agc ctc cag cct gaa gat ttt gca act tac tat tgt ctg cag cat ggt	336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly	
80 85 90	
gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa	381
Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys	
95 100 105	

<210> 96

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "b1" of humanized L
chain V region

<400> 96

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Phe
 20 25 30
 Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
 35 40 45
 Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 97

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<221> sig-peptide

<222> (1)...(60)

<220>

<221> mat-peptide

<222> (61)...(381)

<223> Nucleotide sequence coding for version "b2" of
humanized L chain V region

<400> 97

atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
 -20 -15 -10 -5
 ggg atc cga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct 96
 Gly Ile Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 1 5 10
 gca tct gta gga gac aga gtc acc atc acg tgc aag gcc tca cag gac 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
 15 20 25

```

att aaa agc ttc tta agt tgg tat cag cag aaa cca gag aaa gcc cct 192
Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro
    30                35                40
aag tcc ctg atc tat tat gca act agt ttg gca gat ggg gtc cca tca 240
Lys Ser Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
    45                50                55                60
agg ttc agt ggc tcc gga tct ggt acc gat tac act ctc acc atc tcg 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                65                70                75
agc ctc cag cct gaa gat ttt gca act tac tat tgt ctg cag cat ggt 336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly
                80                85                90
gag agc ccg tac acg ttc ggc gga ggg acc aag gtg gag atc aaa 381
Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                95                100                105

```

<210> 98

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of version "b2" of humanized L chain V region

<400> 98

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1                5                10                15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Lys Ser Phe
                20                25                30
Leu Ser Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
                35                40                45
Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
                50                55                60
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
                65                70                75                80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Tyr
                85                90                95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                100                105

```

<210> 99

<211> 117

<212> PRT

<213> Mouse

<220>

<223> Amino acid sequence of H chain V region of anti TF mouse monoclonal antibody ATR-5

<400> 99

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Thr	Asn	Leu	Val	Arg	Pro	Gly	Ala			
				5					10					15				
Leu	Val	Lys	Leu	Ser	Cys	Lys	Gly	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Tyr			
			20					25					30					
Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile			
		35					40					45						
Gly	Gly	Asn	Asp	Pro	Ala	Asn	Gly	His	Ser	Met	Tyr	Asp	Pro	Lys	Phe			
		50				55					60							
Gln	Gly	Lys	Ala	Ser	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr			
		65			70				75					80				
Leu	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys			
			85					90					95					
Ala	Arg	Asp	Ser	Gly	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser			
		100						105					110					
Val	Thr	Val	Ser	Ser														
				115														

<210> 100

<211> 107

<212> PRT

<213> Mouse

<220>

<223> Amino acid sequence of L chain V region of anti TF mouse monoclonal antibody ATR-5

<400> 100

Asp	Ile	Lys	Met	Thr	Gln	Ser	Pro	Ser	Ser	Met	Tyr	Ala	Ser	Leu	Gly			
				5					10				15					
Glu	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Ile	Lys	Ser	Phe			
			20					25					30					

Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro Lys Thr Leu Ile
 35 40 45
 Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn Asn Leu Glu Ser
 65 70 75 80
 Asp Asp Thr Ala Thr Tyr Tyr Cys Leu Gln His Gly Glu Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 101

<211> 780

<212> DNA

<213> Homosapiens

<220>

<223> DNA coding for soluble human TF

<400> 101

atg gag acc cct gcc tgg ccc cgg gtc ccg cgc ccc gag acc gcc gtc 48
 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
 -30 -25 -20
 gct cgg acg ctc ctg ctc ggc tgg gtc ttc gcc cag gtg gcc ggc gct 96
 Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
 -15 -10 -5 -1
 tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca 144
 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 1 5 10 15
 act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa 192
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 20 25 30
 gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa 240
 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 35 40 45
 tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg 288
 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 50 55 60

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aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca 366
Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
  65                      70                      75                      80
ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac 384
Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
      85                      90                      95
tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca 432
Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
      100                      105                      110
att cag agt ttt gaa cag gtg gga aca aaa gtg aat gtg acc gta gaa 480
Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
      115                      120                      125
gat gaa cgg act tta gtc aga agg aac aac act ttc cta agc ctc cgg 528
Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
      130                      135                      140
gat gtt ttt ggc aag gac tta att tat aca ctt tat tat tgg aaa tct 576
Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
      145                      150                      155                      160
tca agt tca gga aag aaa aca gcc aaa aca aac act aat gag ttt ttg 624
Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
      165                      170                      175
att gat gtg gat aaa gga gaa aac tac tgt ttc agt gtt caa gca gtg 672
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
      180                      185                      190
att ccc tcc cga aca gtt aac cgg aag agt aca gac agc ccg gta gag 720
Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
      195                      200                      205
tgt atg ggc cag gag aaa ggg gaa ttc aga gaa gac tac aaa gac gat 768
Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asp Tyr Lys Asp Asp
      210                      215                      220
gac gat aaa taa 780
Asp Asp Lys
225
<210> 102
<211> 259
<212> PRT
<220>

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<223> Amino acid sequence of soluble human TF

<400> 102

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Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
      -30                -25                -20
Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
      -15                -10                -5                -1
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
   1                5                10                15
Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
      20                25                30
Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
      35                40                45
Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
      50                55                60
Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
      65                70                75                80
Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
      85                90                95
Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
      100                105                110
Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
      115                120                125
Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
      130                135                140
Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
      145                150                155                160
Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
      165                170                175
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
      180                185                190
Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
      195                200                205
Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Asp Tyr Lys Asp Asp
      210                215                220
Asp Asp Lys
225
<210> 103

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<211> 780

<212> DNA

<213> Homosapiens

<220>

<223> DNA coding for human TF

<400> 103

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atg gag acc cct gcc tgg ccc cgg gtc ccg cgc ccc gag acc gcc gtc      48
MET Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
      -30                      -25                      -20

gct cgg acg ctc ctg ctc ggc tgg gtc ttc gcc cag gtg gcc ggc gct      96
Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
      -15                      -10                      -5                      -1

tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca      144
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
      1                      5                      10                      15

act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa      192
Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
      20                      25                      30

gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa      240
Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
      35                      40                      45

tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg      288
Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
      50                      55                      60

aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca      336
Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
      65                      70                      75                      80

ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac      384
Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
      85                      90                      95

tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca      432
Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
      100                      105                      110

att cag agt ttt gaa cag gtg gga aca aaa gtg aat gtg acc gta gaa      480
Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
      115                      120                      125

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gat gaa cgg act tta gtc aga agg aac aac act ttc cta agc ctc cgg      528
Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
      130                      135                      140
gat gtt ttt ggc aag gac tta att tat aca ctt tat tat tgg aaa tct      576
Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
      145                      150                      155                      160
tca agt tca gga aag aaa aca gcc aaa aca aac act aat gag ttt ttg      624
Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
      165                      170                      175
att gat gtg gat aaa gga gaa aac tac tgt ttc agt gtt caa gca gtg      672
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
      180                      185                      190
att ccc tcc cga aca gtt aac cgg aag agt aca gac agc ccg gta gag      720
Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
      195                      200                      205
tgt atg ggc cag gag aaa ggg gaa ttc aga gaa ata ttc tac atc att      768
Cys MET Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile
      210                      215                      220
gga gct gtg gta ttt gtg gtc atc atc ctt gtc atc atc ctg gct ata      816
Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile
      225                      230                      235                      240
tct cta cac aag tgt aga aag gca gga gtg ggg cag agc tgg aag gag      864
Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu
      245                      250                      255
aac tcc cca ctg aat gtt tca taa      888
Asn Ser Pro Leu Asn Val Ser ***
      260

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<210> 104

<211> 259

<212> PRT

<220>

<223> Amino acid sequence of soluble human TF

<400> 104

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MET Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val
      -30                      -25                      -20
Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala
      -15                      -10                      -5                      -1

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Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser
 1 5 10 15
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
 20 25 30
 Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
 35 40 45
 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
 50 55 60
 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
 65 70 75 80
 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
 85 90 95
 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
 100 105 110
 Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu
 115 120 125
 Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg
 130 135 140
 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser
 145 150 155 160
 Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu
 165 170 175
 Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val
 180 185 190
 Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu
 195 200 205
 Cys MET Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile
 210 215 220
 Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile
 225 230 235 240
 Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu
 245 250 255
 Asn Ser Pro Leu Asn Val Ser
 260